

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Emerson, Suzanne U., Purcell, Robert H., Tsarev, Sergei. A., and Robinson, Robin A.
- (ii) TITLE OF INVENTION: Recombinant Proteins Of A Pakistani Strain Of Hepatitis E And Their Use In Diagnostic Methods And Vaccines
- (iii) NUMBER OF SEQUENCES: 111
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORGAN & FINNEGAN
(B) STREET: 345 PARK AVENUE
(C) CITY: NEW YORK
(D) STATE: NEW YORK
(E) COUNTRY: USA
(F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: FLOPPY DISK
(B) COMPUTER: IBM PC COMPATIBLE
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WORDPERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/840,316
(B) FILING DATE: 11-APR-1997
(C) CLASSIFICATION
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Richard W. Bork
(B) REGISTRATION NUMBER: 36,459
(C) REFERENCE/DOCKET NUMBER: 2026-4255
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 758-4800
(B) TELEFAX: (212) 751-6849

(2) INFORMATION FOR SEQ ID NO: 1

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1693 AMINO ACID RESIDUES
(B) TYPE: AMINO ACID
(C) STRANDNESS: UNKNOWN
(D) TOPOLOGY: UNKNOWN
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Glu Ala His Gln Phe Ile Lys Ala Pro Gly Ile Thr Thr Ala
1 5 10 15
Ile Glu Gln Ala Ala Leu Ala Ala Ala Asn Ser Ala Leu Ala Asn
20 25 30

Ala	Val	Val	Val	Arg	Pro	Phe	Leu	Ser	His	Gln	Gln	Ile	Glu	Ile
				35					40					45
Leu	Ile	Asn	Leu	Met	Gln	Pro	Arg	Gln	Leu	Val	Phe	Arg	Pro	Glu
				50					55					60
Val	Phe	Trp	Asn	His	Pro	Ile	Gln	Arg	Val	Ile	His	Asn	Glu	Leu
				65					70					75
Glu	Leu	Tyr	Cys	Arg	Ala	Arg	Ser	Gly	Arg	Cys	Leu	Glu	Ile	Gly
				80					85					90
Ala	His	Pro	Arg	Ser	Ile	Asn	Asp	Asn	Pro	Asn	Val	Val	His	Arg
				95					100					105
Cys	Phe	Leu	Arg	Pro	Ala	Gly	Arg	Asp	Val	Gln	Arg	Trp	Tyr	Thr
				110					115					120
Ala	Pro	Thr	Arg	Gly	Pro	Ala	Ala	Asn	Cys	Arg	Arg	Ser	Ala	Leu
				125					130					135
Arg	Gly	Leu	Pro	Ala	Ala	Asp	Arg	Thr	Tyr	Cys	Phe	Asp	Gly	Phe
				140					145					150
Ser	Gly	Cys	Asn	Phe	Pro	Ala	Glu	Thr	Gly	Ile	Ala	Leu	Tyr	Ser
				155					160					165
Leu	His	Asp	Met	Ser	Pro	Ser	Asp	Val	Ala	Glu	Ala	Met	Phe	Arg
				170					175					180
His	Gly	Met	Thr	Arg	Leu	Tyr	Ala	Ala	Leu	His	Leu	Pro	Pro	Glu
				185					190					195
Val	Leu	Leu	Pro	Pro	Gly	Thr	Tyr	Arg	Thr	Ala	Ser	Tyr	Leu	Leu
				200					205					210
Ile	His	Asp	Gly	Arg	Arg	Val	Val	Val	Thr	Tyr	Glu	Gly	Asp	Thr
				215					220					225
Ser	Ala	Gly	Tyr	Asn	His	Asp	Val	Ser	Asn	Leu	Arg	Ser	Trp	Ile
				230					235					240
Arg	Thr	Thr	Lys	Val	Thr	Gly	Asp	His	Pro	Leu	Val	Ile	Glu	Arg
				245					250					255
Val	Arg	Ala	Ile	Gly	Cys	His	Phe	Val	Leu	Leu	Leu	Thr	Ala	Ala
				260					265					270
Pro	Glu	Pro	Ser	Pro	Met	Pro	Tyr	Val	Pro	Tyr	Pro	Arg	Ser	Thr
				275					280					285
Glu	Val	Tyr	Val	Arg	Ser	Ile	Phe	Gly	Pro	Gly	Gly	Thr	Pro	Ser
				290					295					300
Leu	Phe	Pro	Thr	Ser	Cys	Ser	Thr	Lys	Ser	Thr	Phe	His	Ala	Val
				305					310					315
Pro	Ala	His	Ile	Trp	Asp	Arg	Leu	Met	Leu	Phe	Gly	Ala	Thr	Leu
				320					325					330
Asp	Asp	Gln	Ala	Phe	Cys	Cys	Ser	Arg	Leu	Met	Thr	Tyr	Leu	Arg
				335					340					345

Gly Ile Ser Tyr Lys Val Thr Val Gly Thr Leu Val Ala Asn Glu
 350 355 360
 Gly Trp Asn Ala Ser Glu Asp Ala Leu Thr Ala Val Ile Thr Ala
 365 370 375
 Ala Tyr Leu Thr Ile Cys His Gln Arg Tyr Leu Arg Thr Gln Ala
 380 385 390
 Ile Ser Lys Gly Met Arg Arg Leu Glu Arg Glu His Ala Gln Lys
 395 400 405
 Phe Ile Thr Arg Leu Tyr Ser Trp Leu Phe Glu Lys Ser Gly Arg
 410 415 420
 Asp Tyr Ile Pro Gly Arg Gln Leu Glu Phe Tyr Ala Gln Cys Arg
 425 430 435
 Arg Trp Leu Ser Ala Gly Phe His Leu Asp Pro Arg Val Leu Val
 440 445 450
 Phe Asp Glu Ser Ala Pro Cys His Cys Arg Thr Ala Ile Arg Lys
 455 460 465
 Ala Val Ser Lys Phe Cys Cys Phe Met Lys Trp Leu Gly Gln Glu
 470 475 480
 Cys Thr Cys Phe Leu Gln Pro Ala Glu Gly Val Val Gly Asp Gln
 485 490 495
 Gly His Asp Asn Glu Ala Tyr Glu Gly Ser Asp Val Asp Pro Ala
 500 505 510
 Glu Ser Ala Ile Ser Asp Ile Ser Gly Ser Tyr Val Val Pro Gly
 515 520 525
 Thr Ala Leu Gln Pro Leu Tyr Gln Ala Leu Asp Leu Pro Ala Glu
 530 535 540
 Ile Val Ala Arg Ala Gly Arg Leu Thr Ala Thr Val Lys Val Ser
 545 550 555
 Gln Val Asp Gly Arg Ile Asp Cys Glu Thr Leu Leu Gly Asn Lys
 560 565 570
 Thr Phe Arg Thr Ser Phe Val Asp Gly Ala Val Leu Glu Thr Asn
 575 580 585
 Gly Pro Glu Arg His Asn Leu Ser Phe Asp Ala Ser Gln Ser Thr
 590 595 600
 Met Ala Ala Gly Pro Phe Ser Leu Thr Tyr Ala Ala Ser Ala Ala
 605 610 615
 Gly Leu Glu Val Arg Tyr Val Ala Ala Gly Leu Asp His Arg Ala
 620 625 630
 Val Phe Ala Pro Gly Val Ser Pro Arg Ser Ala Pro Gly Glu Val
 635 640 645
 Thr Ala Phe Cys Ser Ala Leu Tyr Arg Phe Asn Arg Glu Ala Gln
 650 655 660

Arg Leu Ser Leu Thr Gly Asn Phe Trp Phe His Pro Glu Gly Leu
 665 670 675
 Leu Gly Pro Phe Ala Pro Phe Ser Pro Gly His Val Trp Glu Ser
 680 685 690
 Ala Asn Pro Phe Cys Gly Glu Ser Thr Leu Tyr Thr Arg Thr Trp
 695 700 705
 Ser Glu Val Asp Ala Val Pro Ser Pro Ala Gln Pro Asp Leu Gly
 710 715 720
 Phe Thr Ser Glu Pro Ser Ile Pro Ser Arg Ala Ala Thr Pro Thr
 725 730 735
 Pro Ala Ala Pro Leu Pro Pro Pro Ala Pro Asp Pro Ser Pro Thr
 740 745 750
 Leu Ser Ala Pro Ala Arg Gly Glu Pro Ala Pro Gly Ala Thr Ala
 755 760 765
 Arg Ala Pro Ala Ile Thr His Gln Thr Ala Arg His Arg Arg Leu
 770 775 780
 Leu Phe Thr Tyr Pro Asp Gly Ser Lys Val Phe Ala Gly Ser Leu
 785 790 795
 Phe Glu Ser Thr Cys Thr Trp Leu Val Asn Ala Ser Asn Val Asp
 800 805 810
 His Arg Pro Gly Gly Gly Leu Cys His Ala Phe Tyr Gln Arg Tyr
 815 820 825
 Pro Ala Ser Phe Asp Ala Ala Ser Phe Val Met Arg Asp Gly Ala
 830 835 840
 Ala Ala Tyr Thr Leu Thr Pro Arg Pro Ile Ile His Ala Val Ala
 845 850 855
 Pro Asp Tyr Arg Leu Glu His Asn Pro Lys Arg Leu Glu Ala Ala
 860 865 870
 Tyr Arg Glu Thr Cys Ser Arg Leu Gly Thr Ala Ala Tyr Pro Leu
 875 880 885
 Leu Gly Thr Gly Ile Tyr Gln Val Pro Ile Gly Pro Ser Phe Asp
 890 895 900
 Ala Trp Glu Arg Asn His Arg Pro Gly Asp Glu Leu Tyr Leu Pro
 905 910 915
 Glu Leu Ala Ala Arg Trp Phe Glu Ala Asn Arg Pro Thr Cys Pro
 920 925 930
 Thr Leu Thr Ile Thr Glu Asp Val Ala Arg Thr Ala Asn Leu Ala
 935 940 945
 Ile Glu Leu Asp Ser Ala Thr Asp Val Gly Arg Ala Cys Ala Gly
 950 955 960
 Cys Arg Val Thr Pro Gly Val Val Gln Tyr Gln Phe Thr Ala Gly
 965 970 975
 Val Pro Gly Ser Gly Lys Ser Arg Ser Ile Thr Gln Ala Asp Val
 980 985 990

Asp Val Val Val	Val Pro Thr Arg Glu	Leu Arg Asn Ala Trp Arg	995	1000	1005
Arg Arg Gly Phe	Ala Ala Phe Thr Pro	His Thr Ala Ala Arg Val	1010	1015	1020
Thr Gln Gly Arg	Arg Val Val Ile Asp	Glu Ala Pro Ser Leu Pro	1025	1030	1035
Pro His Leu Leu	Leu Leu His Met Gln	Arg Ala Ala Thr Val His	1040	1045	1050
Leu Leu Gly Asp	Pro Asn Gln Ile Pro	Ala Ile Asp Phe Glu His	1055	1060	1065
Ala Gly Leu Val	Pro Ala Ile Arg Pro	Asp Leu Ala Pro Thr Ser	1070	1075	1080
Trp Trp His Val	Thr His Arg Cys Pro	Ala Asp Val Cys Glu Leu	1085	1090	1095
Ile Arg Gly Ala	Tyr Pro Met Ile Gln	Thr Thr Ser Arg Val Leu	1100	1105	1110
Arg Ser Leu Phe	Trp Gly Glu Pro Ala	Val Gly Gln Lys Leu Val	1115	1120	1125
Phe Thr Gln Ala	Ala Lys Ala Ala Asn	Pro Gly Ser Val Thr Val	1130	1135	1140
His Glu Ala Gln	Gly Ala Thr Tyr Thr	Glu Thr Thr Ile Ile Ala	1145	1150	1155
Thr Ala Asp Ala	Arg Gly Leu Ile Gln	Ser Ser Arg Ala His Ala	1160	1165	1170
Ile Val Ala Leu	Thr Arg His Thr Glu	Lys Cys Val Ile Ile Asp	1175	1180	1185
Ala Pro Gly Leu	Leu Arg Glu Val Gly	Ile Ser Asp Ala Ile Val	1190	1195	1200
Asn Asn Phe Phe	Leu Ala Gly Gly Glu	Ile Gly His Gln Arg Pro	1205	1210	1215
Ser Val Ile Pro	Arg Gly Asn Pro Asp	Ala Asn Val Asp Thr Leu	1220	1225	1230
Ala Ala Phe Pro	Pro Ser Cys Glu Ile	Ser Ala Phe His Glu Leu	1235	1240	1245
Ala Glu Glu Leu	Gly His Arg Pro Ala	Pro Val Ala Ala Val Leu	1250	1255	1260
Pro Pro Cys Pro	Glu Leu Glu Gln Gly	Leu Leu Tyr Leu Pro Gln	1265	1270	1275
Glu Leu Thr Thr	Cys Asp Ser Val Val	Thr Phe Glu Leu Thr Asp	1280	1285	1290

Ile Val His Cys Arg Met Ala Ala Pro Ser Gln Arg Lys Ala Val
1295 1300 1305

Leu Ser Thr Leu Val Gly Arg Tyr Gly Arg Arg Thr Lys Leu Tyr
1310 1315 1320

Asn Ala Ser His Ser Asp Val Arg Asp Ser Leu Ala Arg Phe Ile
1325 1330 1335

Pro Ala Ile Gly Pro Val Gln Val Thr Thr Cys Glu Leu Tyr Glu
1340 1345 1350

Leu Glu Glu Ala Met Val Glu Lys Gly Gln Asp Gly Ser Ala Val
1355 1360 1365

Leu Glu Leu Asp Leu Cys Ser Arg Asp Val Ser Arg Ile Thr Phe
1370 1375 1380

Phe Gln Lys Asp Cys Asn Lys Phe Thr Thr Gly Glu Thr Ile Ala
1385 1390 1395

His Gly Lys Val Gly Gln Gly Ile Ser Ala Trp Ser Lys Thr Phe
1400 1405 1410

Cys Ala Leu Phe Gly Pro Trp Phe Arg Ala Ile Glu Lys Ala Ile
1415 1420 1425

Leu Ala Leu Leu Pro Gln Gly Val Phe Tyr Gly Asp Ala Phe Asp
1430 1435 1440

Asp Thr Val Phe Ser Ala Ala Val Ala Ala Ala Lys Ala Ser Met
1445 1450 1455

Val Phe Glu Asn Asp Phe Ser Glu Phe Asp Ser Thr Gln Asn Asn
1460 1465 1470

Phe Ser Leu Gly Leu Glu Cys Ala Ile Met Glu Glu Cys Gly Met
1475 1480 1485

Pro Gln Trp Leu Ile Arg Leu Tyr His Leu Ile Arg Ser Ala Trp
1490 1495 1500

Ile Leu Gln Ala Pro Lys Glu Ser Leu Arg Gly Phe Trp Lys Lys
1505 1510 1515

His Ser Gly Glu Pro Gly Thr Leu Leu Trp Asn Thr Val Trp Asn
1520 1525 1530

Met Ala Val Ile Thr His Cys Tyr Asp Phe Arg Asp Leu Gln Val
1535 1540 1545

Ala Ala Phe Lys Gly Asp Asp Ser Ile Val Leu Cys Ser Glu Tyr
1550 1555 1560

Arg Gln Ser Pro Gly Ala Ala Val Leu Ile Ala Gly Cys Gly Leu
1565 1570 1575

Lys Leu Lys Val Asp Phe Arg Pro Ile Gly Leu Tyr Ala Gly Val
1580 1585 1590

Val Val Ala Pro Gly Leu Gly Ala Leu Pro Asp Val Val Arg Phe
1595 1600 1605

Ala Gly Arg Leu Thr Glu Lys Asn Trp Gly Pro Gly Pro Glu Arg
1610 1615 1620

Ala Glu Gln Leu Arg Leu Ala Val Ser Asp Phe Leu Arg Lys Leu
1625 1630 1635

Thr Asn Val Ala Gln Met Cys Val Asp Val Val Ser Arg Val Tyr
1640 1645 1650

Gly Val Ser Pro Gly Leu Val His Asn Leu Ile Glu Met Leu Gln
1655 1660 1665

Ala Val Ala Asp Gly Lys Ala His Phe Thr Glu Ser Val Lys Pro
1670 1675 1680

Val Leu Asp Leu Thr Asn Ser Ile Leu Cys Arg Val Glu
1685 1690

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 660 amino acid residues
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Pro Arg Pro Ile Leu Leu Leu Leu Leu Met Phe Leu Pro
1 5 10 15

Met Leu Pro Ala Pro Pro Pro Gly Gln Pro Ser Gly Arg Arg Arg
20 25 30

Gly Arg Arg Ser Gly Gly Ser Gly Gly Gly Phe Trp Gly Asp Arg
35 40 45

Val Asp Ser Gln Pro Phe Ala Ile Pro Tyr Ile His Pro Thr Asn
50 55 60

Pro Phe Ala Pro Asp Val Thr Ala Ala Ala Gly Ala Gly Pro Arg
65 70 75

Val Arg Gln Pro Ala Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln
80 85 90

Ala Gln Arg Pro Ala Ala Ala Ser Arg Arg Arg Pro Thr Thr Ala
95 100 105

Gly Ala Ala Pro Leu Thr Ala Val Ala Pro Ala His Asp Thr Pro
110 115 120

Pro Val Pro Asp Val Asp Ser Arg Gly Ala Ile Leu Arg Arg Gln
125 130 135

Tyr Asn Leu Ser Thr Ser Pro Leu Thr Ser Ser Val Ala Thr Gly
140 145 150

Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu Ser Pro Leu Leu Pro
155 160 165

Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala Thr Glu Ala Ser
170 175 180

Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr Ile Arg Tyr Arg
 185 190 195
 Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser Ile Ser
 200 205 210
 Phe Tyr Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp Met Asn
 215 220 225
 Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile
 230 235 240
 Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn
 245 250 255
 Gln Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu Glu Glu
 260 265 270
 Ala Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val
 275 280 285
 Asn Ser Tyr Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu
 290 295 300
 Asp Phe Ala Leu Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn
 305 310 315
 Thr Asn Thr Arg Val Ser Arg Tyr Ser Ser Thr Ala Arg His Arg
 320 325 330
 Leu Arg Arg Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala
 335 340 345
 Ala Thr Arg Phe Met Lys Asp Leu Tyr Phe Thr Ser Thr Asn Gly
 350 355 360
 Val Gly Glu Ile Gly Arg Gly Ile Ala Leu Thr Leu Phe Asn Leu
 365 370 375
 Ala Asp Thr Leu Leu Gly Gly Leu Pro Thr Glu Leu Ile Ser Ser
 380 385 390
 Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro Val Val Ser Ala Asn
 395 400 405
 Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser Val Glu Asn Ala Gln
 410 415 420
 Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile Asp Leu Gly Glu
 425 430 435
 Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His Glu Gln Asp
 440 445 450
 Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser Val Leu
 455 460 465
 Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu Tyr
 470 475 480
 Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Val Ser
 485 490 495

Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val
500 505 510

Ala Arg Ser Leu Asp Trp Thr Lys Val Thr Leu Asp Gly Arg Pro
515 520 525

Leu Ser Thr Ile Gln Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro
530 535 540

Leu Arg Gly Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala
545 550 555

Gly Tyr Pro Tyr Asn Tyr Asn Thr Thr Ala Ser Asp Gln Leu Leu
560 565 570

Val Glu Asn Ala Ala Gly His Arg Val Ala Ile Ser Thr Tyr Thr
575 580 585

Thr Ser Leu Gly Ala Gly Pro Val Ser Ile Ser Ala Val Ala Val
590 595 600

Leu Ala Pro His Ser Val Leu Ala Leu Leu Glu Asp Thr Met Asp
605 610 615

Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro Glu Cys
620 625 630

Arg Pro Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val Ala
635 640 645

Glu Leu Gln Arg Leu Lys Met Lys Val Gly Lys Thr Arg Glu Leu
650 655 660

(2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 123 amino acid residues
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asn Asn Met Ser Phe Ala Ala Pro Met Gly Ser Arg Pro Cys
1 5 10 15

Ala Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys
20 25 30

Cys Pro Arg His Arg Pro Val Ser Arg Leu Ala Ala Val Val Gly
35 40 45

Gly Ala Ala Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu
50 55 60

Ile Leu Ser Pro Ser Gln Ser Pro Ile Phe Ile Gln Pro Thr Pro
65 70 75

Ser Pro Pro Met Ser Pro Leu Arg Pro Gly Leu Asp Leu Val Phe
80 85 90

(2) INFORMATION FOR SEQ ID NO: 4:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

315661 1

125

CAATGAAGGC TGGAACGCCT CTGAGGACGC TCTTACAGCT GTCATCACTG 1150
CCGCCTACCT TACCATCTGC CACCAGCGGT ACCTCCGCAC TCAGGCTATA 1200
TCTAAGGGGA TGCCTCGCCT GGAGCGGGAG CATGCTCAGA AGTTTATAAC 1250
ACGCCTCTAC AGTTGGCTCT TTGAGAAGTC CGGCCGTGAT TATATCCCCG 1300
GCCGTCAGTT GGAGTTCTAC GCTCAGTGTA GGCCTGGCT CTCGGCCGGC 1350
TTTCATCTTG ACCCACGGGT GTTGGTTTTT GATGAGTCGG CCCCTGCCA 1400
CTGTAGGACT GCGATTCTGA AGGCGGTCTC AAAGTTTTGC TGCTTTATGA 1450
AGTGGCTGGG CCAGGAGTGC ACCTGTTTTT TACAACCTGC AGAAGGCGTC 1500
GTTGGCGACC AGGGCCATGA CAACGAGGCC TATGAGGGGT CTGATGTTGA 1550
CCCTGCTGAA TCCGCTATTA GTGACATATC TGGGTCCTAC GTAGTCCCTG 1600
GCACTGCCCT CCAACCGCTT TACCAAGCCC TTGACCTCCC CGCTGAGATT 1650
GTGGCTCGTG CAGGCCGGCT GACCGCCACA GTAAAGGTCT CCCAGGTCGA 1700
CGGGCGGATC GATTGTGAGA CCCTTCTCGG TAATAAAACC TTCCGCACGT 1750
CGTTTGTGTA CGGGGCGGTT TTAGAGACTA ATGGCCCAGA GCGCCACAAT 1800
CTCTCTTTTG ATGCCAGTCA GAGCACTATG GCCGCCGGCC CTTTCAGTCT 1850
CACCTATGCC GCCTCTGCTG CTGGGCTGGA GGTGCGCTAT GTCGCCGCCG 1900
GGCTTGACCA CCGGGCGGTT TTTGCCCCCG GCGTTTCACC CCGGTCAGCC 1950
CCTGGCGAGG TCACCGCCTT CTGTTCTGCC CTATACAGGT TTAATCGCGA 2000
GGCCCAGCGC CTTTCGCTGA CCGGTAATTT TTGGTTCCAT CCTGAGGGGC 2050
TCCTTGCCCC CTTTGCCCCG TTTTCCCCCG GGCATGTTTG GGAGTCGGCT 2100
AATCCATTCT GTGGCGAGAG CACACTTTAC ACCCGCACTT GGTCGGAGGT 2150
TGATGCTGTT CCTAGTCCAG CCCAGCCCGA CTTAGGTTTT ACATCTGAGC 2200
CTTCTATACC TAGTAGGGCC GCCACACCTA CCCCAGCGGC CCCTCTACCC 2250
CCCCCTGCAC CGGATCCTTC CCCTACTCTC TCTGCTCCGG CGCGTGGTGA 2300
GCCGGCTCCT GGCGCTACCG CCAGGGCCCC AGCCATAACC CACCAGACGG 2350
CCCGGCATCG CCGCCTGCTC TTTACCTACC CGGATGGCTC TAAGGTGTTT 2400
GCCGGCTCGC TGTTTGAGTC GACATGTACC TGGCTCGTTA ACGCGTCTAA 2450
TGTTGACCAC CGCCCTGGCG GTGGGCTCTG TCATGCATTT TACCAGAGGT 2500
ACCCCGCCTC CTTTGATGCT GCCTCTTTTG TGATGCGCGA CGGCGCGGCC 2550
GCCTACACAT TAACCCCCCG GCCAATAATT CATGCCGTCG CTCCTGATTA 2600
TAGGTTGGAA CATAACCCAA AGAGGCTTGA GGCTGCCTAC CGGGAGACTT 2650
GCTCCCGCCT CGGTACCGCT GCATACCCAC TCCTCGGGAC CGGCATATAC 2700

CAGGTGCCGA TCGGTCCCAG TTTTGACGCC TGGGAGCGGA ATCACCGCCC 2750
CGGGGACGAG TTGTACCTTC CTGAGCTTGC TGCCAGATGG TTCGAGGCCA 2800
ATAGGCCGAC CTGCCCAACT CTCACTATAA CTGAGGATGT TGCGCGGACA 2850
GCAAATCTGG CTATCGAACT TGA CTCAGCC ACAGACGTCG GCCGGGCCTG 2900
TGCCGGCTGT CGAGTCACCC CCGGCGTTGT GCAGTACCAG TTTACCGCAG 2950
GTGTGCCCTGG ATCCGGCAAG TCCCCTCTA TTACCCAAGC CGACGTGGAC 3000
GTTGTCTGTGG TCCCGACCCG GGAGTTGCGT AATGCCTGGC GCCGCCGCGG 3050
CTTCGCTGCT TTCACCCCGC AACTGCGGC TAGAGTCACC CAGGGGCGCC 3100
GGGTTGTCAT TGATGAGGCC CCGTCCCTTC CCCCTCATTT GCTGCTGCTC 3150
CACATGCAGC GGGCCGCCAC CGTCCACCTT CTTGGCGACC CGAATCAGAT 3200
CCCAGCCATC GATTTTGAGC ACGCCGGGCT CGTTCCCGCC ATCAGGCCCG 3250
ATTTGGCCCC CACCTCCTGG TGGCATGTTA CCCATCGCTG CCCTGCGGAT 3300
GTATGTGAGC TAATCCGCGG CGCATACCCT ATGATTCAGA CCACTAGTCG 3350
GGTCCTCCGG TCGTTGTTCT GGGGTGAGCC CGCCGTTGGG CAGAAGCTAG 3400
TGTTACCCCA GGC GGCTAAG GCCGCCAACC CCGGTTCA GT GACGGTCCAT 3450
GAGGCACAGG GCGCTACCTA CACAGAGACT ACCATCAT TG CCACGGCAGA 3500
TGCTCGAGGC CTCATTCA GT CGTCCCGAGC TCATGCCATT GTTGCCCTGA 3550
CGCGCCACAC TGAGAAGTGC GTCATCAT TG ACGCACCAGG CCTGCTTCGC 3600
GAGGTGGGCA TCTCCGATGC AATCGTTAAT AACTTTTTCC TTGCTGGTGG 3650
CGAAATTGGC CACCAGCGCC CATCTGTTAT CCCTCGCGGC AATCCTGACG 3700
CCAATGTTGA CACCTTGGCT GCCTTCCCGC CGTCTTGCCA GATTAGCGCC 3750
TTCCATCAGT TGGCTGAGGA GCTTGGCCAC AGACCTGCCC CTGTGCGGGC 3800
TGTTCTACCG CCCTGCCCTG AGCTTGAACA GGGCCTTCTC TACCTGCCCC 3850
AAGAACTCAC CACCTGTGAT AGTGTGCTAA CATTTGAATT AACAGATATT 3900
GTGCATTGTC GTATGGCCGC CCCGAGCCAG CGCAAGGCCG TGCTGTCCAC 3950
GCTCGTGGGC CGTTATGGCC GCCGCACAAA GCTCTACAAT GCCTCCCACT 4000
CTGATGTTCTG CGACTCTCTC GCCCGTTTTA TCCCGGCCAT TGGCCCCGTA 4050
CAGGTTACAA CCTGTGAATT GTACGAGCTA GTGGAGGCCA TGGTCGAGAA 4100
GGGCCAGGAC GGCTCCGCCG TCCTTGAGCT CGACCTTTGT AGCCGCGACG 4150
TGTCAGGAT CACCTTCTTC CAGAAAGATT GTAATAAATT CACCACGGGG 4200
GAGACCATCG CCCATGGTAA AGTGGGCCAG GGCATTTCTG CCTGGAGTAA 4250

GACCTTCTGT GCCCTTTTCG GCCCCTGGTT CCGTGCTATT GAGAAGGCTA 4300
TCCTGGCCCT GCTCCCTCAG GGTGTGTTTT ATGGGGATGC CTTTGATGAC 4350
ACCGTCTTCT CGGCGGCTGT GGCCGCAGCA AAGGCATCCA TGGTGTTCTGA 4400
GAATGACTTT TCTGAGTTTG ATTCCACCCA GAATAATTTT TCCTTGGGCC 4450
TAGAGTGTGC TATTATGGAG GAGTGTGGGA TGCCGCAGTG GCTCATCCGC 4500
TTGTACCACC TTATAAGGTC TGCCTGGATT CTGCAGGCCC CGAAGGAGTC 4550
CCTGCGAGGG TTTTGGAAGA AACACTCCGG TGAGCCCGGC ACCCTTCTGT 4600
GGAATACTGT CTGGAACATG GCCGTTATCA CCCACTGTTA TGATTTCCGC 4650
GATCTGCAGG TGGCTGCCTT TAAAGGTGAT GATTCGATAG TGCTTTGCAG 4700
TGAGTACCGT CAGAGCCAG GGGCTGCTGT CCTGATTGCT GGCTGTGGCC 4750
TAAAGTTGAA GGTGGATTTT CGTCCGATTG GTCTGTATGC AGGTGTTGTG 4800
GTGGCCCCCG GCCTTGCGGC GCTTCTGAT GTCTGTGCGT TCGCCGGTCG 4850
GCTTACTGAG AAGAATTGGG GCCCTGGCCC CGAGCGGGCG GAGCAGCTCC 4900
GCCTCGCTGT GAGTGATTTT CTCCGCAAGC TCACGAATGT AGCTCAGATG 4950
TGTGTGGATG TTGTCTCTCG TGTTTATGGG GTTTCCCCTG GGCTCGTTCA 5000
TAACCTGATT GGCATGCTAC AGGCTGTTGC TGATGGCAAG GCTCATTTCA 5050
CTGAGTCAGT GAAGCCAGTG CTTGACCTGA CAAATTCAAT TCTGTGTCGG 5100
GTGGAATGAA TAACATGTCT TTTGCTGCGC CCATGGGTTT GCGACCATGC 5150
GCCCTCGGCC TATTTTGCTG TTGCTCCTCA TGTTTCTGCC TATGCTGCCC 5200
GCGCCACCGC CCGGTCAGCC GTCTGGCCGC CGTCGTGGGC GGCGCAGCGG 5250
CGGTTCCGGC GGTGGTTTCT GGGGTGACCG GGTGATTCT CAGCCCTTCG 5300
CAATCCCCTA TATTCATCCA ACCAACCCTT TCGCCCCGA TGTCACCGCT 5350
GCGGCCGGGG CTGGACCTCG TGTTGCGCAA CCCGCCCGAC CACTCGGCTC 5400
CGCTTGGCGT GACCAGGCC AGCGCCCCGC CGCTGCCTCA CGTCGTAGAC 5450
CTACCACAGC TGGGGCCGCG CCGCTAACCG CGGTCGCTCC GGCCCATGAC 5500
ACCCCGCCAG TGCCTGATGT TGACTCCCGC GGCGCCATCC TGCGCCGGCA 5550
GTATAACCTA TCAACATCTC CCCTCACCTC TTCCGTGGCC ACCGGCACAA 5600
ATTTGGTTCT TTACGCCGCT CCTCTTAGCC CGCTTCTACC CCTCCAGGAC 5650
GGCACCAATA CTCATATAAT GGCTACAGAA GCTTCTAATT ATGCCAGTA 5700
CCGGGTGCT CGTGCCACAA TTCGCTACCG CCCGCTGGTC CCCAACGCTG 5750
TTGGTGGCTA CGCTATCTCC ATTTCTGTTCT GGCCACAGAC CACCACCACC 5800
CCGACGTCCG TTGACATGAA TTCAATAACC TCGACGGATG TCCGTATTTT 5850

AGTCCAGCCC GGCATAGCCT CCGAGCTTGT TATTCCAAGT GAGCGCCTAC 5900
 ACTATCGCAA CCAAGGTTGG CGCTCTGTTG AGACCTCCGG GGTGGCGGAG 5950
 GAGGAGGCCA CCTCTGGTCT TGTCATGCTC TGCATACATG GCTCACCTGT 6000
 AAATTCTTAT ACTAATACAC CCTATACCGG TGCCCTCGGG CTGTTGGACT 6050
 TTGCCCTCGA ACTTGAGTTC CGCAACCTCA CCCCCGGTAA TACCAATACG 6100
 CGGGTCTCGC GTTACTCCAG CACTGCCCCG CACCGCCTTC GTCGCGGTGC 6150
 AGATGGGACT GCCGAGCTCA CCACCACGGC TGCTACTCGC TTCATGAAGG 6200
 ACCTCTATTT TACTAGTACT AATGGTGTG GTGAGATCGG CCGCGGGATA 6250
 GCGCTTACCC TGTTTAACT TGCTGACACC CTGCTTGGCG GTCTACCGAC 6300
 AGAATTGATT TCGTCGGCTG GTGGCCAGCT GTTCTACTCT CGCCCCGTCG 6350
 TCTCAGCCAA TGGCGAGCCG ACTGTAAAGC TGTATACATC TGTGGAGAAT 6400
 GCTCAGCAGG ATAAGGGTAT TGCAATCCCG CATGACATCG ACCTCGGGGA 6450
 ATCCCGTGTA GTTATTCAGG ATTATGACAA CCAACATGAG CAGGACCGAC 6500
 CGACACCTTC CCCAGCCCCA TCGCGTCCCT TTTCTGTCCT CCGAGCTAAC 6550
 GATGTGCTTT GGCTTTCTCT CACCGCTGCC GAGTATGACC AGTCCACTTA 6600
 CGGCTCTTCG ACCGGCCCAG TCTATGTCTC TGA CTCTGTG ACCTTGGTTA 6650
 ATGTTGCGAC CGGCGCGCAG GCCGTTGCCC GGTCACTCGA CTGGACCAAG 6700
 GTCACACTTG ATGGTCGCCC CCTTTCCACC ATCCAGCAGT ATTCAAAGAC 6750
 CTTCTTTGTC CTGCCGCTCC GCGGTAAGCT CTCCTTTTGG GAGGCAGGAA 6800
 CTAATAAGC CGGGTACCCT TATAATTATA ACACCACTGC TAGTGACCAA 6850
 CTGCTCGTTG AGAATGCCGC TGGGCATCGG GTTGCTATTT CCACCTACAC 6900
 TACTAGCCTG GGTGCTGGCC CCGTCTCTAT TTCCGCGGTT GCTGTTTTAG 6950
 CCCCCACTC TGTGCTAGCA TTGCTTGAGG ATACCATGGA CTACCCTGCC 7000
 CGCGCCCATC CTTTCGATGA CTTCTGCCCC GAGTGCCGCC CCCTTGGCCT 7050
 CCAGGGTTGT GCTTTTCAGT CTA CTGTGCGC TGAGCTTCAG CGCCTTAAGA 7100
 TGAAGGTGGG TAAACTCGG GAGTTATAGT TTATTTGCTT GTGCCCCCT 7150
 TCTTTCTGTT GCTTATTT 7168

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACATTTGAAT TCACAGACAT TGTGC

25

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ACACAGATCT GAGCTACATT CGTGAG

26

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAAGGGATCC ATGGTGTTTG AGAATG

26

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACTCACTGCA GAGCACTATC GAATC

25

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGTAAACTG GTACTGCACA AC

22

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAGTCCCGCT CTATTACCCA AG

22

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ACCCACGGGT GTTGTTTTT G

21

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTCTTGGGGC AGGTAGAGAA G

21

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTATTGAATT CATGTCAACG GACGTC

26

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATAATTCAT GCCGTCGCTC C

21

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAGCTCAGGA AGGTACAACT C 21

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAATCGATGG CTGGGATCTG ATTC 24

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAGGCATTGT AGAGCTTTGT G 21

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GATGTTGCAC GGACAGCAAA TC 22

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATCTCCGATG CAATCGTTAA TAAC 24

(2) INFORMATION FOR SEQ ID NO: 20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TAATCCATTC TGTGGCGAGA G 21

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AAGTGTGACC TTGGTCCAGT C

21

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTGCTCGTGC CACAATTCGC TAC

23

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CATTTCACTG AGTCAGTGAA G

21

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

TAATTATAAC ACCACTGCTA G

21

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GATTGCAATA CCCTTATCCT G

21

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATTAAACCTG TATAGGGCAG AAC

23

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AAGTTCGATA GCCAGATTTG C

21

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TCATGTTGGT TGTCATAATC C

21

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATGACGCAC TTCTCAGTGT G

21

(2) INFORMATION FOR SEQ ID NO: 30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AGAACAACGA ACGGAGAAC

19

(2) INFORMATION FOR SEQ ID NO: 31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AGATCCCAGC CATCGACTTT G 21

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TAGTAGTGTA GGTGGAAATA G 21

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GTGTGGTTAT TCAGGATTAT G 21

(2) INFORMATION FOR SEQ ID NO: 34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ACTCTGTGAC CTTGGTTAAT G 21

(2) INFORMATION FOR SEQ ID NO: 35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AACTCAAGTT CGAGGGCAAA G 21

(2) INFORMATION FOR SEQ ID NO: 36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGCTTACCCT GTTTAACCTT G

21

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATCCCCTATA TTCATCCAAC CAAC

24

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CTCCTCATGT TTCTGCCTAT G

21

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCCAGAACGA AATGGAGATA GC

22

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTCAGACATA AAACCTAAGT C

21

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

136

TGCCCTATAC AGGTTTAATC G

21

(2) INFORMATION FOR SEQ ID NO: 42:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACCGGCATAT ACCAGGTGC

19

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATGGCTCA CTCGTAAATT C

21

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

AACATTAGAC GCGTTAACGA G

21

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTCTTTTGAT GCCAGTCAGA G

21

(2) INFORMATION FOR SEQ ID NO: 46:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACCTACCCGG ATGGCTCTAA GG

22

137

(2) INFORMATION FOR SEQ ID NO: 47:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

TATGGGAATT CGTGCCGTCC TGAAG

25

(2) INFORMATION FOR SEQ ID NO: 48:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

AGTGGGAGCA GTATACCAGC G

21

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CTGCTATTGA GCAGGCTGCT C

21

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGGCCATTAG TCTCTAAAAC C

21

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GAGGTTTTCT GGAATCATC

19

(2) INFORMATION FOR SEQ ID NO: 52:

a1

138

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GCATAGGTGA GACTG

15

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AGTTACAGCC AGAAAACC

18

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCATGGATCC TCGGCCTATT TTGCTGTTGC TCC

33

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGGCAGACCA CATATGTG

18

(2) INFORMATION FOR SEQ ID NO: 56:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGTGCACTCC TGACCAAGCC

20

(2) INFORMATION FOR SEQ ID NO: 57:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ATTGGCTGCC ACTTTGTTC

19

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACCCTCATAC GTCACCACAA C

21

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GCGGTGGACC ACATTAGGAT TATC

24

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

CATGATATGT CACCATCTG

19

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GTCATCCATA ACGAGCTGG

19

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid

a1

140

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

AGCGGAATTC GAGGGGCGGC ATAAAGAACC AGG 33

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCGCTGAATT CGGATCACAA GCTCAGAGGC TATGCC 36

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GTATAACGGA TCCACATCTC CCCTTACCTC 30

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

TAACCTGGAT CCTTATGCCG CCCCTCTTAG 30

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

AAATTGGATC CTGTGTCGGG TGGAATGAAT AACATGTC 38

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 37 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ATCGGCAGAT CTGATAGAGC GGGGACTTGC CGGATCC

37

(2) INFORMATION FOR SEQ ID NO: 68:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

TACCCGTGCCC GCGCCCATAC TTTTGATG

28

(2) INFORMATION FOR SEQ ID NO: 69:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GGCTGAGATC TGGTTCGGGT CGCCAAGAAG GTG

33

(2) INFORMATION FOR SEQ ID NO: 70:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TACAGATCTA TACAACTTAA CAGTCGG

27

(2) INFORMATION FOR SEQ ID NO: 71:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GCGGCAGATC TCACCGACAC CATTAGTAC

29

(2) INFORMATION FOR SEQ ID NO: 72:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCGTCGGATC CCAGGGGCTG CTGTCCTG

28

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AAAGGAATTC AAGACCAGAG GTAGCCTCCT C

31

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GTGATATGA ATTCAATAAC CTCGACGG

28

(2) INFORMATION FOR SEQ ID NO: 75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

TTTGGATCCT CAGGGAGCGC GGAACGCAGA AATGAG

36

(2) INFORMATION FOR SEQ ID NO: 76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

TCACTCGTGA ATTCCTATAC TAATAC

26

(2) INFORMATION FOR SEQ ID NO: 77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 34 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

TTTGGATCCT CAGGGAGCGC GGAACGCAGA AATG

34

143

(2) INFORMATION FOR SEQ ID NO: 78:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

TGATAGAGCG GGACTTGCCG GATCC

25

(2) INFORMATION FOR SEQ ID NO: 79:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TTGCATTAGG TTAATGAGGA TCTC

24

(2) INFORMATION FOR SEQ ID NO: 80:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACCTGCTTCC TTCAGCCTGC AGAAG

25

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GCGGTGGATC CGCTCCCAGG CGTCAAAAC

29

(2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GGGCGGATCG AATTCGAGAC CCTTCTTGG

29

(2) INFORMATION FOR SEQ ID NO: 83:

ai

144

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

AGGATGGATC CATAAGTTAC CGATCAG

27

(2) INFORMATION FOR SEQ ID NO: 84:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GGCTGGAATT CCTCTGAGGA CGCCCTCAC

29

(2) INFORMATION FOR SEQ ID NO: 85:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GCCGAAGATC TATCGGACAT AGACCTC

27

(2) INFORMATION FOR SEQ ID NO: 86:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

CAGACGACGG ATCCCCTTGG ATATAGCCTG

30

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 40 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGCCGAATTC AGGCAGACCA CATATGTGGT CGATGCCATG

40

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs

ai

145

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GCAGGTGTGC CTGGATCCGG CAAGT 25

(2) INFORMATION FOR SEQ ID NO: 89:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GTTAGAATTTC CGGCCCAGCT GTGGTAGGTC 30

(2) INFORMATION FOR SEQ ID NO: 90:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

CCGTCCGATT GGTCTGTATG CAGG 24

(2) INFORMATION FOR SEQ ID NO: 91:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

TACCAGTTTA CTGCAGGTGT GC 22

(2) INFORMATION FOR SEQ ID NO: 92:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

CAAGCCGATG TGGACGTTGT CG 22

(2) INFORMATION FOR SEQ ID NO: 93:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GGCGCTGGGC CTGGTCACGC CAAG 24

(2) INFORMATION FOR SEQ ID NO: 94:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GCAGAAACTA GTGTTGACCC AG 22

(2) INFORMATION FOR SEQ ID NO: 95:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

TAGGTCTACG ACGTGAGGCA AC 22

(2) INFORMATION FOR SEQ ID NO: 96:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

TACAATCTTT CAGGAAGAAG G 21

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

CCCACACTCC TCCATAATAG C 21

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GATAGTGCTT TGCAGTGAGT ACCG

24

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTATAACGGA TCCACATCTC CCCTTACCTC

30

a₁
(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

TACAGATCTA TACAACCTAA CAGTCGG

27

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GCGGCAGATC TCACCGACAC CATTAGTAC

29

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TAACCTGGAT CCTTATGCCG CCCCTCTTAG

30

(2) INFORMATION FOR SEQ ID NO: 103:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GCACAACCTA GGTTACTATA ACTCCCGAGT TTTACC

36

(2) INFORMATION FOR SEQ ID NO: 104:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GGGTTCCCTA GGATGCGCCC TCGGCCTATT TTG

33

(2) INFORMATION FOR SEQ ID NO: 105:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

CGTGGGCCCTA GGAGCGGCGG TTCCGGCGGT GGT

33

(2) INFORMATION FOR SEQ ID NO: 106:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GCTTGGCCTA GGCAGGCCCA GCGCCCCGCC GCT

33

(2) INFORMATION FOR SEQ ID NO: 107:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CCGCCACCTA GGGATGTTGA CTCCGCGGC GCC

33

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

TTCGGATCCA TGGCGGTCGC TCCGGCC

27

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 33 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

TCAAGCTTAT CATCATAGCA CAGAGTGGGG GGC

33

(2) INFORMATION FOR SEQ ID NO: 110

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 AMINO ACID RESIDUES
(B) TYPE: AMINO ACID
(C) STRANDNESS: UNKNOWN
(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

Ala Ala Pro Leu Thr Ala Val Ala Pro Ala His Asp Thr Pro Pro
5 10 15
Val Pro Asp Val Asp
20

(2) INFORMATION FOR SEQ ID NO: 111

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 AMINO ACID RESIDUES
(B) TYPE: AMINO ACID
(C) STRANDNESS: UNKNOWN
(D) TOPOLOGY: UNKNOWN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

Ala Ala Pro Leu Thr Ala Val Ala Pro Ala His Asp Thr Pro Pro
5 10 15
Val Pro Asp Val Asp
20

150